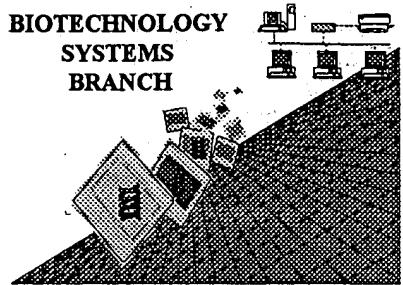


# **RAW SEQUENCE LISTING**

## **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:**

Application Serial Number: 09/147,801  
Art Unit / Team No.: 1643 BATCA  
Date Processed by STIC: 2/7/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED   SUGGESTED   CORRECTION

SERIAL NUMBER: 09/142,801

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos   The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4  Misaligned Amino Acid Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length   Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7  PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8  Skipped Sequences (OLD RULES)   Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES)   Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**

10  Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11  Use of <213>Organism (NEW RULES)   Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.

12  Use of <220>Feature (NEW RULES)   Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13  PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

### **INPUT SET: S32460.raw**

**This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

All item 5  
on Error  
summary sheet

## SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: ~~↑ move up - all responses~~ Does Not Comply *leads*  
Corrected Diskette Needed

(A) NAME: BO NIKLASSON  
(B) STREET: ~~Sibyllegatan 15~~  
(C) CITY: ~~Stockholm~~  
(D) COUNTRY: ~~Sweden~~  
(E) POSTAL CODE (ZIP): ~~114 42~~

(ii) TITLE OF INVENTION: NEW PICORNAVIRUSES, VACCINES AND DIAGNOSTIC KITS

(iii) NUMBER OF SEQUENCES: 4

(v) (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0

(M) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE:  
(B) STREET:  
(C) CITY:  
(D) STATE:  
(E) COUNTRY:  
(F) ZIP:

ERUSES, VACCINES AND DIAGNOSTIC KITS  
add these mandatory headings and

← add headings and responses

response  
for a U.S.  
filed

## **ERRORED SEQUENCES FOLLOW:**

57 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Picornaviridae  
(C) INDIVIDUAL ISOLATE: Ljungan 174F

INPUT SET: S32460.raw

73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
74  
75 AGTCTAGTTT CATTCTGTGT GTGTTGGCA CTGAAATTAT TTCTGTCTCT GGGGTGCTTT 60  
76  
77 ACACCTCAGT AGGGGCTGTA CCCGGGCGGT CCCACTCTTC ACAGGAATTG CACAGGTGGC 120  
78  
79 TTTCACCTCT GGACAGTGCA TTCCACACCC GCTCCACAGT AGAAGATGAT GTGTGTCTTT 180  
80  
81 GCTTGTGAAA AGCTTGTGAA AATCGTGTGT AGGCGTAGCG GTACTTGAGT GCCAGCGGAC 240  
82  
83 ACCCCTAGTG GTAACACTAG C 261  
84  
85  
--> 86 (2) INFORMATION FOR SEQ ID NO: 3:  
87 ↑  
88 (i) SEQUENCE CHARACTERISTICS:  
89 (A) LENGTH: 264 base pairs 263 shown  
90 (B) TYPE: nucleic acid  
91 (C) STRANDEDNESS: single  
92 (D) TOPOLOGY: unknown  
93  
94 (ii) MOLECULE TYPE: cDNA to mRNA  
95  
96 (iii) HYPOTHETICAL: NO  
97  
98 (vi) ORIGINAL SOURCE:  
99 (A) ORGANISM: Picornaviridae  
100 (C) INDIVIDUAL ISOLATE: Ljungan 145SL  
101  
--> 102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
103  
104 AGTTTGGTTC TCTCTTGAGT GTGTTTGAGT TTAGCATAAT TTCTGTCTCT AGAGTGCTTT 60  
105  
--> 106 ACACCTCAGT AGGGGCTGTA CCCGGGCGGT CCCACTCTTC ACAGGAATCT GCACAGGTG 120 119  
107  
108 CTTTCACCTC TGGACAGTGC ATTCCATACC CGCTCCACAA TAGAAGATGA TGTATATCTT 180 179  
109  
110 TGTTTGTGAA ATGCTCATGA AACGTGTGTG TAGGGCGTAGC GGCTACTTGA ATGCCAGCGG 240 239  
111  
112 AACCCCCCTA GTGGTAACAC TAGC 264 263  
113

--OK

---

114 (2) INFORMATION FOR SEQ ID NO: 4:  
115  
116 (i) SEQUENCE CHARACTERISTICS:  
117 (A) LENGTH: 179 amino acids  
118 (B) TYPE: amino acid  
119 (C) STRANDEDNESS:  
120 (D) TOPOLOGY: unknown  
121  
122 (ii) MOLECULE TYPE: peptide  
123  
124 (iii) HYPOTHETICAL: NO

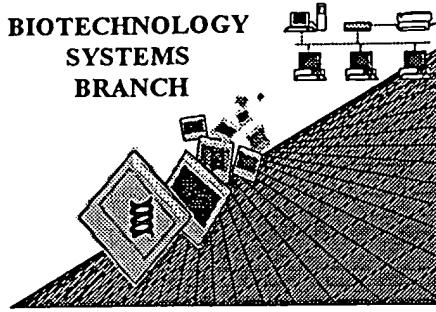
all next page

INPUT SET: S32460.raw

125  
126 (v) FRAGMENT TYPE: internal  
127  
128 (vi) ORIGINAL SOURCE:  
129 (A) ORGANISM: Picornaviridae  
130 (C) INDIVIDUAL ISOLATE: Ljungan 145SL  
131  
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
133  
134 Lys Asp Leu Met Glu Ile Ala Arg Met Pro Ser Val Tyr Lys Gly Glu  
135 1 5 10 15  
136  
137 Arg Thr Glu Pro Gly Gly Thr Asn Gly Tyr Phe Gln Trp Ser His Thr  
138 20 25 30  
139  
140 His Ser Pro Ile Asn Trp Val Phe Asp Gly Gly Ile His Leu Glu Asp  
141 35 40 45  
142  
143 Met Pro Asn Leu Asn Leu Phe Ser Ser Cys Tyr Asn Tyr Trp Arg Gly  
144 50 55 60  
145  
146 Ser Thr Val Leu Lys Leu Thr Val Tyr Ala Ser Thr Phe Asn Lys Gly  
147 65 70 75 80  
148  
149 Arg Leu Arg Met Ala Phe Phe Pro Ile Met Met Gln Gly Thr Gln Arg  
150 85 90 95  
151  
152 Lys Lys His Lys Cys Leu Phe Met Val Cys Asp Ile Gly Leu Asn Asn  
153 100 105 110  
154  
155 Thr Phe Glu Met Thr Ile Pro Tyr Thr Trp Gly Asn Trp Met Arg Pro  
156 115 120 125  
157  
158 Thr Arg Gly Ser Val Ile Gly Trp Leu Arg Ile Asp Val Leu Asn Arg  
159 130 135 140  
160  
161 Leu Thr Tyr Asn Ser Ser Pro Asn Ala Val Asn Cys Ile Leu Gln  
162 145 150 155 160  
163  
164 Val Lys Met Gly Asn Asp Ala Lys Phe Met Val Pro Thr Thr Ser Asn  
165 165 170 175  
166  
167 Ile Val Trp  
168 27  
169  
170  
171  
172 *delete at end of file*

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/147,801**
**INPUT SET: S32460.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: BO NIKLASSON
7	Unknown or Misplaced Identifier	(B) STREET: Sibyllegatan 15
8	Unknown or Misplaced Identifier	(C) CITY: Stockholm
9	Unknown or Misplaced Identifier	(E) COUNTRY: Sweden
10	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 114 42
15	Number of Sequences (4) Doesn't Equal Actual Count (3)	(iii) NUMBER OF SEQUENCES: 4
60	Entered (261) and Calc. Seq. Length (271) differ	(A) LENGTH: 261 base pairs
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	Wrong Nucleic Acid Designator	2) INFORMATION FOR SEQ ID NO: 3:
86	# of Sequences for line conflicts w/ running total	(A) LENGTH: 264 base pairs
89	Entered (264) and Calc. Seq. Length (263) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
102	Wrong Sequence Number	ACACTCTAGT AGGGGCTGTA CCCGGGCGGT CCCAC
106	# of Sequences for line conflicts w/ running total	(2) INFORMATION FOR SEQ ID NO: 4:
114	Sequence 3 missing	



## Notice of Availability of Checker Program

### Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>  
The software is in current directory: pub/checker/  
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441  
WASHINGTON DC 20231

**COST FOR DISKETTE IS \$ 25.00**

**METHOD OF PAYMENT:**

Check payable to Commissioner of Patents and Trademarks

VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737

PTO Deposit Account

*For Further Information, Contact: Arti Shah at 703-308-4212*

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other:

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**